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October 21, 2005, 07:10:04; Search time 134 Seconds (without alignments) 5461.655 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Description	Sequence 2, Appli	Sequence 4, Appli	Sequence 8, Appli	Sequence 3, Appli	Ξ,	13,	Sequence 14, Appl	15,	Sequence 6, Appli	Sequence 10, Appl	Sequence 16, Appl
ΩΙ	US-10-719-385-2	US-10-719-385-4	US-10-719-385-8	US-10-719-385-3	US-10-719-385-11	US-10-719-385-13	US-10-719-385-14	US-10-719-385-15	US-10-719-385-6	US-10-719-385-10	US-10-719-385-16
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Score	9007	9005	9008	9004	9004	9004	9004	9003	9002	9002	9001
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29	292.5		2013	18	US-10-756-149-5015	5015,
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33	176.5	5.0	2902	16	0-437-963-154	Seguence 154118,
34	175.5	•	1676	14	-10-128-714	Sequence 8246, Ap
35	169.5		2621	16	3-437-963-12216	Sequence 122168,
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37	165	1.8	1545	14	0-128-714	Sequence 3246, Ap
38	160.5		2462	16	US-10-437-963-114113	114113
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GENERAL INFORMATION:

APPLICANT: O'Toole et al.

TITLE OF INVENTION: Composition and Method for Treating Lupus Nephritis

FILE REFERENCE: 22058-582

CURRENT APPLICATION NUMBER: US/10/719,385

CURRENT APPLICATION NUMBER: OCT/US03/37339

PRIOR APPLICATION NUMBER: PCT/US03/37339

PRIOR PILING DATE: 2003-11-21

PRIOR PILING DATE: 2003-11-21

PRIOR PILING DATE: 2002-11-21

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 2.2
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100.0%; Pred. No. 0;
tive 0; Mismatches
Publication No. US20040209284A1
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Best Local Similarity 100.
Matches 1753; Conservative
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; ORGANISM: Homo sapiens
US-10-719-385-2
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121 OSOALILKIADYYYEERTCILKCVLHLITYRODERHPYRVBYADCVDKLEKELVSKYROQ 180 121 OSOALILKIADYYYEERTCILKCVLHLITYRODERHPYRVBYADCVDKLEKELVSKYROQ 180 122 OSOALILKADDYYYEERTCILKCVLHLITYRODERHPYRVBYADCVDKLEKELVSKYROQ 180 123 DSOALILKIADYYYEERTCILKOVHATTROSHLITTEITTYYYERARPSDLIVIT 240 124 KWFKEQGFGSRQTNBHLVDETMDFFVDRIGYESALILVEGMDIESLHKCALDDRRELHQF 300 241 KWFKEQGFGSRQTNBHLVDETMDFFVDRIGYESALILVEGMDIESLHKCALDDRRELHQF 300 241 KWFKEQGFGSRQTNBHLVDETMDFFVDRIGYESALILVEGMDIESLHKCALDDRRELHQF 300 241 KWFKEQGFGSRQTNBHLVDETMDFFVDRIGYESALILVEGMDIESLHKCALDDRRELHQF 300 301 AQDGLICQDMDCLMLTFGDIPHHAPVLLAMALLRHTLNPEETSSVVRKIGGTAIQLNVFQ 360 301 AQDGLICQDMDCLMLTFGDIPHHAPVLLAMALLRHTLNPEETSSVVRKIGGTAIQLNVFQ 360 301 AQDGLICQDMDCLMLTFGDIPHAPVLLAMALLRHTLNPEETSSVVRKIGGTAIQLNVFQ 360 301 AQDGLICQDMDCLMLTFGDIPHAPVLLAMALLRHTLNPEETSSVVRKIGGTAIQLNVFQ 360 301 AQDGLICQDMDCLMLTFGDIPHAPVLLAMALLRHTLANDGDIIPHACALDDRRELHQF 300 421 PELFWGTEPTSGLGIILDSVCGMPPHLLSPLLQLLRALVSGKSTAKKVYSFLDKWSFYNE 480 421 PELFWGTEPTSGLGIILDSVCGMPPHLSPLLQLLRALVSGKSTAKKVYSFLDKWSFYNE 480 421 PELFWGTEPTSGLGIILDSVCGMPPHLSPLLQLLRALTTGDLYNTATTGDLYNTATTGTDLYNTATTGTDLYNTATTGTDLYNTATTGTDLYNTATTGTDLYNTATTGTDLYNTATTGTDLYNTATTGTDLYNTATTGTDLYNTATTGTDLYNTATTGTDLYNTATTGTDLYNTATTGTDLYNTATTGTDLYNTATTGTDL	721 SYHKWRYNSHGVREQIGCLILELIHAIINLCHETDLHSSHTPSLOFLCICSLAYTEAGOT 780 721 SYHKWRYNSHGVREQIGCLILELIHAIINLCHETDLHSSHTPSLOFLCICSLAYTEAGOT 780 721 SYHKWRYNSHGVREQIGCLILELIHAILNLCHETDLHSSHTPSLOFLCICSLAYTEAGOT 780 781 VINIMGIGVDTIDMYMAAOPRSDCAEGOGOGOLIKTVKLAFSYTNNVIRLKPPSNVYSP 840 781 VINIMGIGVDTIDMYMAAOPRSDCAEGOGOGOLIKTVKLAFSYTNNVIRLKPPSNVYSP 840 841 LEQALSQHGAHGNNLIAVLAKYIYHKHDPALPRIAIQLIKRLATVAPMSYYACLGNDAAA 900 841 LEQALSQHGAHGNNLIAVLAKYIYHKHDPALPRIAIQLIKRLATVAPMSYYACLGNDAAA 900 901 IRDAFLTRLOSKIEDMRIKWMILEFLTVAVETOPGLIELFINLEVKDGSDGSKEFSLGMW 960 901 IRDAFLTRLOSKIEDMRIKWMILEFLTVAVESLDOSLANLYRTKPKFWENLTSP 1020 1021 LFGTLSPPSETSEPSILETCALIMKIICLEITYYVKGSLDOSLANLYRTKFKFFWENLTSP 1080 1021 LFGTLSPPSETSEPSILETCALIMKIICLEITYYVKGSLDOSLANLYRKERFFWENLTSP 1080 1081 GYVKSLAVHVAETEGSSCTSLLEYQMLVSAWRULLITATTHADIMHLTRSVVRRQLFLDV 1140 1141 LDGTKALLLVPASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGFUTFILEGVLQADQ 1200 1141 LDGTKALLLVPASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGFUTFILEGVLQADQ 1200 1141 LDGTKALLLVPASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGFUTFILEGVLQADQ 1200 1120 QLMEKTKAKVPSAFITVLQMKEBKVSDIPQYSQLVLNVCETLQSSVTBLILEGTLGFUTPALGOND 1200 1121 LDGTKALLLVPASVNCLRLGSMKCTLLLILLRQWKRELGSSVDEILGFUTPLTELLGTGVLQADQ 1200 1121 LDGTKALLLVPASVNCLRLGSMKCTLLLILLRQWKRELGSSVDEILGFUTPLTELLGTGVLQADQ 1200 1121 LDGTKALLTVPASVNCLRLGSMCTLLLILLLARGNYRELGSSVDEILGFUTPLTELLILLARGNYRELGSSVDEILGFUTPLTELLILLARGNYRELGSSVDEILGFUTPLTELLILLARGNYRCHLGSWKCTLLLILLARGNYRELGSSVDEILGFUTPLTTLLILLARGNYRCHLGSWKTLLLILLARGNYRCHLGSWKRELGSSVDEILGFUTPLTTLLILLARGNYRCHLGSWKTLLGSWCTLLLILLARGNYRCHLGSWKRELGSSVDEILGFUTPLTTLLILLARGNYRCHLGSWKTLUTPLTTLLILLARGNYRCHLGSWCTLALLTLLILLARGNYRCHLGSWKTLARA

1201 1201 1261 1261 1321 1321			Db 1621 ALNMICGELDKKKEPLTGAVGLSTQAEGTRTLKELLM Qy 1681 PRDKQRWKQELSSELSTLLSSLSRYFRRGAPSSPAT Db 1681 PRDKQRWKQELSSELSTLLSSLSRYFRRGAPSSPAT Qy 1741 IQLVQAFVRHMQR 1753 Db 1741 IQLVQAFVRHMQR 1753	RESULT 3 US-10-719-385-8 Sequence 8, Application US/10719385 Fublication No. US20040209284A1 GENERAL INFORMATION: TITLE OF INVENTION: FILE REFERENCE: 22058-582 CURRENT FILING DATE: 2003-11-21 PRIOR APPLICATION NUMBER: 2003-11-21 PRIOR APPLICATION NUMBER: PCT/US03/37339	PRIOR APPLIANCE JOURNEERS: 60/428, 094 ; PRIOR APPLICATION UNDBERS: 60/428, 094 ; PRIOR FILING DATE: 2002-11-21 ; NUMBER OF SEQ ID NOS: 26 ; SOFTWARE: PatentIN Ver. 2.1 ; SEQ ID NO 8 ; LENGTH: 1753 ; TYPE: PRT ; ORGANISM: HOMO Sapiens US-10-719-385-8	Query Match
121 QSQALILKIADYYYEBRTCILRCVLHLLTYFQDERHPYRUEYADCVDKLEKELVSKYRQQ 180 121 QSQALILKIADYYYEBRTCILRCVLHLLTYFQDERHPYRUEYADCVDKLEKELVSKYRQQ 180 181 FEELYKTEAPTWETHGNLMTERQVSRWFVQCLREQSMLLEIIFLYXAYFBMABSDLLVLT 240 181 FEELYKTEAPTWETHGNIMTERQVSRWFVQCLREQSMLLEIIFLYXAYFBMABSDLLVLT 240 241 KMFKEQGFGSRQTNRHLVDETMDFFVDRIGYFSALILVBGMDIESLHKCALDDRRELHQF 300 241 KMFKEQGFGSRQTNRHLVDETMDPFVDRIGYFSALILVBGMDIESLHKCALDDRRELHQF 300 241 KMFKEQGFGSRQTNRHLVDETMDPFVDRIGYFSALILVBGMDIESLHKCALDDRRELHQF 300	301 AQDGLICQDMDCLMLFFGDIPHHAPVLLAWALLRHTLNPEETSSVVRKIGGTAIQLNVFQ 360	421 PELFWGTEPTSGLGIILDSVCGMFPHLLSPLLQLLRALVSGKGTAKKVYSFLDKMSFYNE 480  421 PELFWGTEPTSGLGIILDSVCGMFPHLLSPLLQLLRALVSGKSTAKKVYSFLDKMSFYNE 480  481 LYKHKPHDVISHEDGTLWRRQTPKLLYPLGGGTNLRIPQGTVGQVMLDDRAYLVRWEYSY 540  481 LYKHKPHDVISHEDGTLWRRQTPKLLYPLGGGTNLRIPQGTVGQVMLDDRAYLVRWEYSY 540  481 LYKHKPHDVISHEDGTLWRRQTPKLLYPLGGGTNLRIPQGTVGQVMLDDRAYLVRWEYSY 540  541 SSWTLFTCEIEMLLHVVSTADVIQHCQRVXFIIDLVHKVISTDLSIADCLLPITSRIYML 600		721 SYHKWRYNSHGVREQIGCLILELIHAILMLCHETDLHSSHTPSLQFLCICSLAYTEAGOT 780	901 IRDAFLTRLOSKIEDMRIKVMILEFLTVAVETOPGLIELFLALEVKDGSDGSKEFSLGMW 960	1021 LFGTLSPPSETSEPSILETCALIMKIICLEIYYVVKGSLDQSLKDTLKKFSIEKRFAYWS 1080  1081 GYVKSLAVHVAETEGSSCTSLLEYQMLVSAWRMLLITATTHADIMHLTDSVVRQLFLDV 1140  1081 GYVKSLAVHVVAETEGSSCTSLLEYQMLVSAWRMLLITATTHADIMHLTDSVVRQLFLDV 1140  1141 LDGTKALLLVPASVNCLRLGSMKCTLLLLLRQWKRELGSVDEILGPLTEILEGVLQADQ 1200  1141 LDGTKALLLVPASVNCLRLGSMKCTLLLLLRQWKRELGSVDEILGPLTEILEGVLQADQ 1200  1141 LDGTKALLLVPASVNCLRLGSMKCTLLLLLLRQWKRELGSVDEILGPLTEILEGVLQADQ 1200
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; Publication No. US20040209284A1
; GENERAL INFORMATION:
   TITLE OF INVENTION: Composition and Method for TITLE OF INVENTION: Composition and Method for FILE REPERENCE: 22058-582
   CURRENT PAPLICATION NUMBER: US/10/719,385
   CURRENT FILING DATE: 2003-11-21
   PRIOR APPLICATION NUMBER: PCT/US03/37339
   PRIOR FILING DATE: 2003-11-21
   PRIOR APPLICATION NUMBER: 60/428,094
   PRIOR FILING DATE: 2002-11-21
   NUMBER OF SEQ ID NOS: 26
   SOFTWARE: PALENTIN Ver. 2.1
   SEQ ID NO 13
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ORGANISM: Homo
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US-10-719-385-13
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1	721 SYHKWRYNSHGYREGIGGLILELIHAILALCHEDLHSSHTPSLQFLCILSLATFAGGT 780 721 SYHKWRYNSHGYREGIGGLILELIHAILALCHEDLHSSHTPSLQFLCILSLAYTEAGGT 780 721 SYHKWRYNSHGYREGIGGLILELIHAILALCHETDLHSSHTPSLQFLCICSLAYTEAGGT 780 781 VINIMGIGVDTIDMVWAAQPRSDGAEGGGGGLLIKTVKLAFSVTNNVIRLKPPSNNVSP 840 1841 LEQALSCHGAHGNNLIAVLAKYIYHKHDPALPRLAIQLIKTLAFSVTNNVIRLKPPSNNVSP 840 1841 LEQALSCHGAHGNNLIAVLAKYIYHKHDPALPRLAIQLIKTVALAFSVTNNVIRLKPPSNNVSP 840 1841 LEQALSCHGAHGNNLIAVLAKYIYHKHDPALPRLAIQLIKTLATVAPMSVYACLGNDAA 900 901 IRDAFLTRLQSKIEDMRIKVMILEFLTVAVETQPGLIELFLNLEVKDGSDGSKEFSLGMW 960 901 IRDAFLTRLQSKIEDMRIKVMILEFLTVAVETQPGLIELFLNLEVKDGSDGSKEFSLGMW 960 901 IRDAFLTRLQSKIEDMRIKVMILEPLTVAVETQPGLIELFLNLEVKDGSDGSKEFSLGMW 960 901 IRDAFLTRLQSKIEDMRIKVMILEPLTVAVETQPGLIELFLNLEVKDGSDGSKEFSLGMW 960 901 IRDAFLTRLQSKIEDMRIKVMILEPLTVAVETQPGLIELFLNLEVKDGSDGSKEFSLGMW 960 901 IRDAFLTRLQSKIEDMRIKVMILEPLTVAVETQPGLIELFLNLEVKDGSDGSKEFSLGMW 960 901 IRDAFLTRLQSKIEDMRIKVMILEPLTVAVETQPGLIELFLALMQDRRDSAMLVLRTKFKFKFMNLTSP 1020 1021 LEGTLASPPSETSEPSILETCALIMRAIAFLHALWQDRRDSAMLVLRTKFKFKFMNLTSP 1020 1021 LEGTLASPPSETSEPSILETCALIMRIICLEIYXVVKGSLDQSLKDTLKKFSIEKRFAVWS 1080 1021 LEGTLASPPSETSERSILETCALIMKIICLEIYXVVKGSLDQSLKDTLKKFSIEKRFAVWS 1080
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Sequence 18, Application US/10719385;
Publication No. US2004020284A1
GENERAL INFORMATION:
APPLICANTON: Composition and Method for Treating Lupus Nephritis
TITLE OF INVENTION: Composition and Method for Treating Lupus Nephritis
FILE REFERENCE: 22058-582
CURRENT APPLICATION NUMBER: US/10/719,385
CURRENT FILING DATE: 2003-11.21
PRIOR PILING DATE: 2003-11.21
PRIOR PLICATION NUMBER: FCT/US03/37339
PRIOR PILING DATE: 2003-11.21
PRIOR PILING DATE: 2003-11.21
NUMBER: 60/428,094
PRIOR FILING DATE: 2002-11-21
SEQ ID NO 18
LENGTH: 1753
TYPE: PATENTH 1753
TYPE: PATENTH HOMO Sapiens
US-10-719-385-18
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US-10-719-385-9
Sequence 9, Application US/10719385
Sequence 9, Application US/10719385
Publication No. US20040209284A1
GENERAL INFORMATION:
TITLE OF INVENTION: Composition and Method for TITLE OF INVENTION: Composition and Method for FILE REFERENCE: 22058-582
CURRENT APPLICATION NUMBER: US/10/719,385
CURRENT FILING DATE: 2003-11-21
PRIOR FILING DATE: 2003-11-21
PRIOR FILING DATE: 2003-11-21
PRIOR FILING DATE: 2002-11-21
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SOFTWARE: Patentin Ver. 3
SEQ ID NO 9
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Sequence 813, App
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Sequence 526, App
Sequence 1515, App
Sequence 1515, App
Sequence 480, App
Sequence 1511, App
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Sequence 40265, Application US/10450763

GENERAL INFORMATION:

APPLICANT: Hyeeq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

CURRENT APPLICATION NUMBER: US/10/450,763

CURRENT FILING DATE: 2003-06-11

PRIOR FILING DATE: 2001-03-30

PRIOR FILING DATE: 2001-03-31

PRIOR FILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736

SEQ ID NO 40265
                                 US-60-701-052-816
US-60-701-052-816
US-60-701-057-318
US-60-701-057-318
US-60-717-196-1217
US-60-717-196-1219
US-60-717-252-524
US-60-717-252-524
US-60-717-252-524
US-60-717-252-524
US-11-222-021-1513
US-11-222-021-1513
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Pred. No. 0;
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Best Local Similarity 99.1
Matches 1727; Conservative
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ORGANISM: Homo sapiens
US-10-450-763-40265
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1: /cgn2 6/pcodata/2/paa/PCT NEW COMB.pep:*

2: /cgn2 6/ptodata/2/paa/US06 NEW COMB.pep:*

3: /cgn2 6/ptodata/2/paa/US07 NEW COMB.pep:*

4: /cgn2 6/ptodata/2/paa/US08 NEW COMB.pep:*

5: /cgn2 6/ptodata/2/paa/US08 NEW COMB.pep:*

6: /cgn2 6/ptodata/2/paa/US10 NEW COMB.pep:*

7: /cgn2 6/ptodata/2/paa/US11 NEW COMB.pep:*

8: /cgn2 6/ptodata/2/paa/US11 NEW COMB.pep:*
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Compugen Ltd.
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US-60-717-251-660
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US-60-717-251-661
US-60-717-251-663
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                          PSAVAQRVQRPPSAASAAPSSSKQPAADTEASEQQALHTVQYGLLKILSKTLAALRHFTP
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100.0%; Pred. No. 8e-27;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION TO CONTROLL OF THE SECOND STATE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES FILLS REPERENCE: 790(TP3/US CURRENT APPLICATION NUMBER: US/10/450,763 CURRENT FILING DATE: 2003-06-11 PRIOR PELICATION NUMBER: 10F7/US01/08631 PRIOR PELICATION NUMBER: 09/540,217 PRIOR PELICATION NUMBER: 09/640,167 PRIOR PELICATION NUMBER: 09/649,167 PRIOR FILING DATE: 2000-03-31 PRIOR FILING DATE: 2000-03-31 PRIOR FILING DATE: 2000-03-31 PRIOR FILING DATE: 2000-03-31 PRIOR FILING DATE: 2000-08-23 NUMBER OF SEQ ID NOS: 60736 SEQ ID NOS: 60736 SEQ ID NOS: 60736 LENGTH: 100
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GENERAL INFORMATION:
TAPLICANT: JOSELOFF, Elizabeth et al.
TITLE OF INVERTION: KIDNEY DISEASE TARGETS AND USES THEREOF FILE REFERENCE: CLOO1591
CURRENT APPLICATION UNMBER: US/60/664,936
CURRENT FILING DATE: 2005-03-25
NUMBER OF SEQ ID NOS: 2456
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8.210-450-763-40264
; Sequence 40264, Application US/10450763
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 90; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 535 --KVNGSSHVENIQGAGGSP-----VSWEHPFHSLMLYH---EHLRKDLPSADSVQY 581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         691 ----LNEIESRCEEYPLTRAFCQLISTLVESSFPSNLGAGLRPPGFDPYLQFLRDSVFL 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYHKWRYNSHGVREQIGCLILELIHAILNLCHETDLHSSHTPSL-----OFLCICS---L 772
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                                                                                                                                                                                                                         -----ISKFLGLDBEQSVQLLQC--YLQEDYRG-TRDSVKTVLQDERQSQALIL 127
                                                                                                                                                                                                                                                                                                                                                                                                       226 YAYFEMAPSDLLVLTKMFKEQGFGSRQTNRHLVDETMDP--FVDRIGYFSALILVEGMDI 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------ESLHKCALDDRRE----LHQFAQDGLICQDMDCLMLTFGDIPH-HAPVL 327
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                                                                                                                                                                                                                                                                                    KIADYYYEBRICILRCVLHIL-------TYFODERHPYRVEYADCVD
                                                                                                                                                                 41 NKHWRRLLEG------LSYYK--PPSPSSAEKV-KANKDVASPLKELGLR-
                                                                                                                                     Gaps
                                                                                                                                   Indels 741;
                                                                                                        DB 8; Length 2012;
                                                                                                        Query Match
3.2%; Score 292.5; DB 8;
Best Local Similarity 18.9%; Pred. No. 7.2e-13;
Matches 416; Conservative 303; Mismatches 743;
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 325
LENGTH: 2012
                                               TYPE: PRT
ORGANISM: Homo sapiens
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US-60-664-936-325
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qq	797	AYKPPGFSLMYHLLNESPMLELALSLLEEGVKQLD-TYAPPPGKKHLEKAVQHCLALLNL 855
ò	819	KL-AFSVTNNVIRLKPPSNVVSPLEQALSQHGAHGNNLIAVLAKXIXHKHDPALPRL 874
Db	856	TLQKENIFMDILRESQLALIVCPLEQLLQGINPRTKKADNVNI-ARYLYHGNTNPEL 912
È	875	AIQLLKRLATVAPMS
qq	913	A FESPAKILCCISCNSNIQIKLVGDFTHDQSISQKLMAGFVECLDCEDAEBFVRLEEGSEL 972
ò	910	QSKIEDMRIKVWILEFLTVANETQPGLIELF-LNLEVKDGSDGSKEFSLGMWSC 962
Db	973	EKKLVAIRHETRIHILMILITSLECNPPNLALYLIGFELKKPVSTTNLQDPGVLGCPRTC 1032
γ̈́ο	963	LHAVLELIDSQQDRYWCPPLLHRAAIAFLHALMQDRRDSAMLVLRTKPKF 1013
Db	1033	LHAILNILEKGTEGRTGPVAVRESPQLAELCYQVIYQLCACSDTSGPTMRYLRTSQDF 1090
ò	1014	WENLTSPLEGTLSPPSETS-EPSILETCALIMKIICLEIYYVVKGSLDQSLKDT 1066
οp	1001	
È	1067	LKKFSIEKRFAVWSGY
Dp	1141	HLLLDDMPVKPYSDGEGGİEDENRSVSĞFLHFDTATKVRRKILNILDSIDFSQEIPEPLQ 1200
È	1083	SSCT 1099
QQ	1201	LDFFDRAQIEQVIANCEHKNLRGQTVCNVKLLHRVLVAEVNALQGMAAIGQRPLLMEBIS 1260
ć	1100	
q	1261	TVLOYVVGRNKLLQCLHAKRHALESWRQLVEIİLTACPQDLIQAEDRQLIIRDILQDVHD 1320
δ	1141	LDGTKALLLVPASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGP 1187
Op	1321	KILDDEAAQELMPVVAGATSVLGPABAHYAFMLDS 1373
ò	1188	
QQ	1374	CFTSPPPEENPLVGFASIGDSSLYIILKKLLDFILKTGGG-FQRVRTHLYGSLLYYLQIA 1432
ò	1222	Æ
qq	1433	GRPDEPDTLEAAKKTWWERLTAPEDVFSKLQRENIAIIESYGAALMEVVCRDAC 1486
È	1270	ETDDCSRSRHRDQRDGVCVLGLHLAXELCEVDEDGDSWLQVTRRLPILPTLLTTLEVSLR 1329
qq	1487	DGHEIGRMLALALIDRIVSVDKQ-QQWLLYLSNSGYLKVLVDSLVEDDR 1534
δ	1330	MKQNLHFTEATLHLLITLARTQQGATAVAGAGITQSICLPLLSVYQLST 1378
a a	1535	TLÓSLLTPQPPLLKALYTYBSKMAFLTRVAKIQQGALBLLRSGVIVRLAQCQVYDMRP 1592
à	1379	NGTAQTPSASR-KSLDAPSWPGVYRLSMSLMBQLLKTLRYNFLPBALDFVGVHQ 1431
ą	1593	ETDPOSMFGMRDPPMFIPTPVDRYRQILLPALQLCQVILTSSWAQHLQAAGQVLQFLISH 1652
ò	1432	ERTLQCLNAVRIVQSLACLEBADHTVGFILQLSNFMKEWHFHLPQLMRDIQVNLGYLC 1489
qq	1653	SDIIQAILRCODV-SAGSLQELALLTGIISKAALPGILSELDVDVNEGSLM 1702
δλ	1490	QACTSLIHSRKWLQHYLQHXLQBCLPSAVAQRVQRPPSAASAAPSS 1535
qq	1703	ELQGHIGRFQRQCLGLLSRFGGSDRLRQFKFQDDNVEGDKV 1743
ò	1536	LKILSKTLAALRHFTPDVCQILLDQSLDI     -
q	1744	SKKDEIEL-AMQQICANVMEYCQSLMLQSSPTFQHA 1778
ò	1596	LSFTTPTFDSEVMLG 1626
DP	1779	VCLFTPSLSETVNRDGPRQDTQAPVVPYWRLPGLGIIIYLLKQSANDFFSYYDSHRQSVS 1838

Db 508 TIYIPYLKMLQGLANGPQCAHYCFSLL	OY 566 CORVKPIIDLVHKVISTDLSIADCLLPITSRIYMLLQRLTTVISPPVDVIASCVN 620	621	Qy 666 GYGNLIANSEQPQGEYGVTIAFLRLITTIVKGQLGSTQSQGLVPCVMFVLKEMLP 720	Qy 721 SYHKWRYNSHGVREQIGCLILELIHAILNLCHETDLHSSHTPSLQFLCICSL 772	Qy 773 AYTEAG	CY 819 KL-AFSVTNNVIRLKPPSNVVSPLEQALSQHGAHGNNLIAVLAKYIYHKHDPALPRL 874    ::	QY 875 AIQLLKRLATVAPMSVYACLGNDAAAIRDAFLTRL 909	Qy 910 QSKIEDDMRIKVMILEFLITVAVETOPGLIELF-LALEVKDGSDGSKEFSLGMMSC 962 :  :	QY 963 LHAVLELIDSQQDRYWCPPLLHRAAIAFLHALWQDRRDSAMLVLRTKPKF 1013	QY 1014 WENLTSPLFGTLSPPSETS-EPSILETCALIMKIICLEIYYVVKGSLDQSLKDT 1066  Db 1091LPSQLQYLPFSNKEYEISMLNQMSWLMKTASIELRVTSLNRQRSHTQRLL 1140	1067 1141 HLLI	QY 1083SSCT 1099  LOI LDFFDRAQIEQVIANCEHKNLRGQTVCNVKLLHRVLVAEVNALQGMAAIGQRPLLMEEIS 1260	RRQLFLDV   :    IRDILQDVHD	1141LDGTKALLLVPASVNCLRLGSM 	1188	1433 QRPDEPDTLEAAKKTWWERLTAPEDVFSKLQRENIALIESYGAALMEVUCRDAC	Qy 1270 ETDDCSRSRHRDQRDGVCVLGLHLAKELCEVDEDGDSWLQVTRRLPILFTLLFTLEVSLK 1329  1487 E :
1627 ELDKKKEPLTQAVGLSTQAEGTRTLKSLLMFTM :	UY 1660 ENCETLLISQAMKIRDPANIPROKQKMRQELSSELSTLLISSELSTERKGAPSSEATG 1/1/	Qy 1718 VLPSPQGKSTSLSKASPESQEPLIQLVQAFVRHMQR 1753  Db 1943ETNLDFRSGLAIVSQHDLDQLQADAINAFGESLQK 1977	RESULT 4 US-60-701-038-305 ; Sequence 305, Application US/60701038	; GENERAL INFORMATION: ; APPLICANT JOSELOFF, Elizabeth et al. ; TITLE OF INVENTION: KIDNEY DISEASE TARGETS AND USES THEREOF ; FILE REFERENCE: CLOO1616	; CURRENT APPLICATION NUMBER: US/60/701,038 ; CURRENT FILING DATE: 2005-07-21 ; NUMBER OF SEQ ID NOS: 1828 ; SOFTWARE: FastSEQ for Windows Version 4.0	ິດ	2%; Score 292.5; DB 8; Length 2012; 9%; Pred. No. 7.2e-13;	ALI NKHWRRLLEGLSYYKPPSPSSAEKV-KANKDVASPLKELGLR	26 NALWRRQPEAVHLLDKILKKHKPPFISLFKNPPKNVQQHEKVQKASTEGVAIQGGGGTRL  82ISKFLGLDEEQSVQLLQCYLQEDYRG-TRDSVKTVLQDERQSQALIL :   :   :   :   :   :   :	D5 86 LPEQLIKEAFILSDLFDIGELAAVELLLAGEHQQPHFPGLTRGLVAVL 134  Qy 128 KIADYYYEERTCILRCVLHLLTYFQDERHPYRVEYADCVD 167	Db 135YWDGKRCIANSLKALIQSRRGKTWTLELSPELASMTTRFTDELMEQGLTYKVLT- 188  Qy 168 KLEKELVSKYRQOPEELYKTEAPTWETHONLMTERQVSRWFVQCLREQSMLLEIIFLY 225  Db 160	226 YAYPEMAPSDLLVLTKMFKEQGFGSRQTNRHLVDETMDPFVDRIGYFSALILVEGMDI	DD Z36 ACQSPUGKEDTLLLIGHLEKVIVEANGSLUAVNLALLAVLLATLTFDI 281  QY 284ESLHKCALDDRRELHQFAQDGLICQDMDCLMLTFGDIPH-HAPVL 327  Dh 282 CPIEGGTEERDDMTHOLDITTEROYTATTHSRIAM	328 LAWALLRHTLNPEETSSVVRKIGGTALQLNVFQYLTRLLQSLASGGNDCTTST	Qy 381 ACMCVYGLLSFVLTSLELHTLGNQQDIIDTACEVLADPSLP 421	Qy 422	QY 446 HILSPILQILRALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWRRQTPKL 505

1333 WGNI	Db 189LVSQIDVNNEFEKLQRERGLGSEKH- Qy 226 YAYFEMAPSDLLVLTKMPKEQGFGSRQTURH		Db 282 SFIEGSTEERDDMIHQLPLLTEKQYIATIHS  Qy 328 LAWALLRHTLNPEETSSVVKKIGG	Qy 381 ACMCVYGLLSFVLTSLBLHTLGNQQD Db 388 YIRNJHWIJTDFLALMPMKVKOLRNRADBDA	4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	DD 448 ELYKAPFHLELALEYRCFIEFLGIFIINGS Qy 446 HLLSPLGLLRALVSGKSTAKKVYSFLDKMS :     :   :     :	Qy 506 LYPLGGQTNLRIPQGTVGQVMLDDRAYLVRW	566 CQRVKPIIDLWHKVISTDLSIADCL	621	Qy 666 GYGNLLMNSEQPQGEYGVTIAFLLITTLUK	Qy 721 SYHKMRYNSHGVREQIGCLILELIHAILNLC   : :  ::     746 RFRTRAYRRABEKWEVAEVVLEVFYKLLR	Qy 773 AYTEAGQTVINIMGIGV	Qy 819 KL-AFSVTNNVIRLKPPSNVVSPLEQAL   ::::  :          Db 856 TLQKENLFMDLLRESQLALIVCFLEQLLQGI	Qy 875 AIQLAKRLATVAPMS	Qy 910 QSKIEDWRIKVMILEFLTVAVETQPGLIE ;	Qy 963 LHAVLELIDSQQQDRYWCPPLLHRAAIAFLH	Qy 1014 WENLTSPLEGTLSPPSETS-EPSILETCA	Qy 1067LKKFSIEKRFAYWSGY
0100 0 1002	MKQNLHFTEATLHLLTLARTQQGATAVAGAGITQSICLFLLSVYQLST	TLQSLLTPQPPLLKALYTYESRVAFLTRVAKIQQGALELLRSGVIVRLAQCQVYDMRP NGTAQTPSASR-KSLDAPSWPGVYRLSMSLMEQLLKTLRYNFLPEALDFVGVHQ	ERTLQCLNAVRTVQSLACLEEADHTVGFILQLSNFMKEWHFHLPQLMRDIQVNLGYLC	QACTSLLHSRKMLQHYLQNKNGDGLPSAVAQRVQRPPSAASAAPSS :	SKQPAADTEASEQOALHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLAEYNFLFA	LSFTTPTFDSEVMLG :     :     : :     : :     : :     : : :     : : :     : : :     : : :     : : :     : : :     : : : :     : : : :     : : : : :     : : : :   : : : : : :   : : : : :   : : : : : : : :   : : : : : : : : : : : :   :	ELDKKKEPLTQAVGLSTQAEGTRTLKSLIMFTM :	ENCFYLLISQAMRYLRDPAVHPRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATG	VLPSPQGKSTSL-  :   :	pplication US/	SKERAL INFORMATION: APPLICANT: Steven RUBEN et al. TITLE OF INVENTION: BREAST DISEASE TARGETS AND USES THEREOF FILE REFERENCE: CL001624	CURRENT APPLICATION NUMBER: US/60/717,251 CURRENT FILING DATE: 2005-09-16 NUMBER OF SEQ ID NOS: 1966 SOFTWARE: FastSEQ for Windows Version 4.0	EQ ID NO 660 LENGTH: 2012 TYPE: PRT ORGANISM: Homo sapiens	-660 3.2%; Score 292.5; DB 8; Length 2012; Similarity 18.9%; Pred. No. 7.2e-13; 12.01	41b; COMBETVACIVE 503; MISMACCHEB 745; INCERS 741; GAPS 41 NGHWRRLEGLSYYKPPSPSSAEKV-KANKDVASPLKELGLR-	ISKFLGLDEEQSVQLQCYLQEDYRG-TRDSVKTVLQDERQSQALIL	LPEQLIKEAFILSDLFDIGELAAVELLLAGEHQQPHFPGLTRGLVAVLL	YMDGKKCIANSLKALIQSKKGKIWILELBFELASMITKFIDELMEGGLIITVUI- KLEKELVSKYRQQFEELYKTEAPTWETHGNLMTERQVSRWFVQCLREGSMLLEIIFLY     :     :   :   :   :   :   :   :   :
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AELCYQVIYQLCACSDTSGPTMRYLRTSQDF 1090 HALWQ------DRRDSAMLVLRTKPKF 1013 CALIMKIICLEIYYVVKGSLDQSLKDT---- 1066 ::|| :|: ### SWLMKTASIELRVT---SLNRQRSHTQRLL 1140 CHFDTATKVRRKILNILDSIDFSQEIPEPLQ 1200 ELF-LNLEVKDGSDGSKEFSLGMW----SC 962 4----RKEVSDLIKEC---RQSLAESLFAW 235 || |:: :|: | |:: :| :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| |:: :| IQFAQDGLICQDMDCLMLTFGDIPH-HAPVL 327 GTAIQLNVFQYLTRLLQSLASGGNDCTTST 380 --IIDTACEVLADPSLP------ 421 ASFYNELYKHKPHDVISHEDGTLWRRQTPKL 505 534 WEYSYSSWILFICEIEMLLHVVSTADVIQH 565 SRIYMLLQ--RLTTVISP---PVDVIASCVN 620 STITWSENAKLALCEHPOWTPVVVILGLLO 635 DLRHTGFLPFVAHPVSSLSQMISAEGMNAG 665 TKGQLGSTQSQGL----VPCVMFVLKEMLP 720 CHETDLHSSHTPSL----OFLCICS---L 772 WDTIDMVMAAQPRSDGAEGQGQGGLIKTV 818 3VKQLD-TYAPPBGKKHLEKAVQHCLALLNL 855 -----VYACLGNDAAA--IRDAFLTRL 909 HLVDETMDP--FVDRIGYFSALILVEGMDI SGLG-----PILDSVCGMF----P

104;

Gaps

741;

82 81

188

283 281

us-10-719-385-2.rapn

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346 RFRTRAYRRAAEKWEVAEVVLEVFYKLLR------DYSEPQLEDFVDQFVELQGEEII 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        282 SFIEGSTEERDDMIHQLPLLTEKQYIATIHSRLQDSQLWK------LPGLQATVR 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |: |: | :: | 388 YIRRVHNLITDFLALMPMKVKQLRNRADEDARMIHMSMQMGNEPPISLRRDLEHLMLIG 447
                                                                                                                                                                                                                                -----ISKFLGLDEEQSVQLLQC--YLQEDYRG-TRDSVXTVLQDERQSQALIL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ESLHKCALDDRRE----LHQFAQDGLICQDMDCLMLTFGDIPH-HAPVL 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAWALLRHTLN--PE----ETSSVVRKIGGTAIQLNVFQYLTRLLQSLASGGNDCTTST 380
                                                                                                                                                                                                                                                                                                                                                                                    566 CQRVKPIIDLVHKVISTDLSIADCLLPITSRIYMLLQ--RLTTVISP---PVDVIASCVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----LINEIESRCEEYPLITRAFCQLISTLVESSFPSNLGAGLRPPGFDPYLQFLRDSVFL
                                                                                                                                                                                                 26 NALWRROPĖAVHLLDKILKKHKPDFISLFKNPPKNVQQHĖKVOKASTEGVAIQGQGGTRL
                                                                                                                                                                                                                                                                                                   KIADYYYEERTCILRCVLHLL-------TYFQDERHPYRVEYADCVD
                                                                                                                                                                                                                                                                                                                                ----YWDGKRCIANSLKALIQSRRGKTWTLELSPELASMTTRFTDELMEQGLTYKVLT-
                                                                                                                                                                                                                                                                                                                                                                 168 KLEKELVSK--YRQOFEELYKTEAPTWETHGNLMTEROVSRWFVQCLREQSMLLEIIFLY
                                                                                                                                                                                                                                                                                                                                                                                                                                 226 YAYFEMAPSDLLVLTKMFKEQGFGSRQTNRHLVDETMDP--FVDRIGYFSALILVEGMDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------ELFWGTEPT----SGLG-----IILDSVCGMF----P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 446 HILSPLIQLIRALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWRRQTPKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        506 LYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSWTLFTCEIEMLLHVVSTADVIQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --RHLPSRGITQK--EQDGLIA--FLQLTSTIITWSENARLALCEHPQWTPVVVILGLLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-----LTVLAA--RNP---AKVWTDLRHTGFLPFVAHPVSSLSQMISAEGMNAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       666 GYGNLLMNSEQPQGEYGVTIAFLRLITTLVKGQLGSTQSQGL-----VPCVMFVLKEMLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYHKWRYNSHGVREQIGCLILELIHAILNLCHETDLHSSHTPSL----QFLCICS---L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----LSYYK--PPSPSSAEKV-KANKDVASPLKELGLR-
                                                                                                  Length 2012;
                                                                                                                                                                                                                                                               86 LPEQLIKEAFILSDLFDIGELAAVELLLAGEHQOPHFPGLTRGLVAVLL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   381 ACMCVYGLLS -- FVLTSLELHTLGNOOD -- -- IIDTACEVLADPSLP-
                                                                                                                                 Indels
                                                                                                1.2%; Score 292.5; DB 8; al Similarity 18.9%; Pred. No. 7.2e-13; 416; Conservative 303; Mismatches 743;
                                                                                                                                                                   41 NKHWRRLLEG----
               ; LENGTH: 2012
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-717-196-497
SEQ ID NO 497
                                                                                                   Query Match
Best Local S:
Matches 416
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                                                                                                                   1261 TVLQYVVGRNKLLQCLHAKRHALESWRQLVEIILTACPQDLIQAEDRQLIIRDILQDVHD 1320
                                                                                                                                                                                                                                        E-----MKVSDIPQYSQLVL--NVCETLQEEVIALFDQTRHSLALGSATED---KDSM 1269
                                                                                                                                                                                                                                                                                                                  ORPDEPDILEAAKKIMWERLTAPEDVFSKLORENIAIIE-----SYGAALMEVVCRDAC 1486
                                                                                                                                                                                                                                                                                                                                                                                                                                         |: | : | : : | : ETDPQSMFGMRDPPMFIPTPVDRYRQILLPALQLCQVILTSSMAQHLQAAGQVLQFLISH 1652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1653 SDTIQAILRCQDV-SAGSLQELALLTGIISKAA-----LPGILSELDVDVNEGSLM 1702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q------ACTSLLH----SRKMLQHYLQNKNGDGLPSAVAQRVQRPPSAASAAPSS 1535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKQPAADTEASEQQALHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLAEYNFLFA 1595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----SPTFQHÀ 1778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VCLFTPSLSETVNRDGPRQDTQAPVVPYWRLPGLGIIIYLLKQSANDFFSYYDSHRQSVS 1838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLONVEQLPPDEIKE-LCÓSVMPAGVDKISTAQKYVLARRRLVKVINNRAKLLSLCSFII 1897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENCFYLLISQAMRYLRDPAVH--PRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATG 1717
                                                                                                                                                                                                                     ------LTEILEGVLQADQQLMEKTKAKVFSAFITVLQMK 1221
                                                                                                                                                                       1487 DGHBIGR-------MLALALLDRIVSVDKQ-QQWLLYLSNSGYLKVLVDSLVEDDR
                                                                                                                                                                                                                                                                                                                                                   ETDDCSRSRHRDQRDGVCVLGLHLAKELCEVDEDGDSWLQVTRRLPILPTLLTTLEVSLR
                                                                                                                                                                                                                                                                                                                                                                                                                      1330 MKQN------LHFTEATLHLLLTLARTQQGATAVAGAGITQSICLPLLSVYQLST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERTLQCLNAVRTVQSLACLEEADHTVGFILQLSNFMKEWHFHLPQLMR--DIQVNLGYLC
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                                                                                                                                                    --LDGTKALLLVPASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1379 NGTAQTPSASR-KSLDAPSWPGVYRLSMSLMEQLLKTLRYNFLPEALDFVG-----VHQ
                                                                                    ---QMLVSAWRML--LIIATTHADIMHLTD-SVVRRQLFLDV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----APSFGTLLATVNVALN----
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GENERAL INFORMATION:
APPLICANT: Mehdi MESRI et al.
TITLE OF INVENTION: STOWACH DISEASE TARGETS AND USES THEREOF
FILE REFERENCE: CLOO1631
CURRENT APPLICATION NUMBER: US/60/717,196
CURRENT PILING DATE: 2005-09-16
NUMBER OF SEQ ID NOS: 2826
SOFTWARE: FASELSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLPSPQGKSTSL---SKASPESQEPLIQL----VQAFVRHMQR 1753
                    -VKSL-AVHVAETEG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : | : | : | | : | : | ELQGHIGRFQRQCLGLLSRFGGSDRLRQFKFQDDNVEG-
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Qy 1627 ELDKKKEPLTQAV  1839 KLQNVEQLPPDBIKE-LCQSVMPAGVD  Qy 1660 ENCFYLLISQAMRYLRDPAVHPRDK    Db 1898 ETCLFILWRHLEYYLHCMPTDS  Qy 1718 VLPSPQGKSTSLSKASPESQEPLI    Db 1943ETNLDFRSGLAIVSQHDLD	RESULT 7 US-60-701-038-306 Sequence 306, Application US/60701038 SEGUENCE 306, Application US/60701038 STILE OF INVENTION: KIDNEY DISEASE TARE FILE REFERENCE: CLO01616 CURRENT APPLICATION NUMBER: US/60/701, CURRENT FILING DATE: 2005-07-21 NUMBER OF SEQ ID NOS: 1828 SOFTWARE: FastSEQ for Windows Version SEQ ID NO 306 LENGTH: 2013 TYPE: PRT TYPE: PRT  CORANISM: HOMO Sapien8	Query Match Query Match Best Local Similarity 18.9%; Pred: N Matches 416; Conservative 303; Mism Qy 41 NKHWRRLLEG	Qy   82ISKFLGLDEEGSVQLL	Qy         226 YAYPEMAPSDILVLTKMFKEQGFGSRQ           b         236 ACQSPLGKEDTLLLI           Qy         284ESLHKCALDDRRE           b         282 SFIEQSTEERDDMIHQLPLLTEKQYIA           Qy         328 LAWALLRHTLNPEFTSSVVR	DD 331 LAWALALRGISQLPDVTALAEFTEADE  Qy 381 ACMCVYGLLSFVLTSLELHTLGNQQ  382 YIRVHNLITDFLALMPMKVKQLRNRA  Qy 422ELFWGTEPT  DD 448 ELYKOPPHLELALEYWCPTEPLQTPT  QY 446 HLLSPLLQLLRALVSGKSTAKKYSFL  DD 508 TIXIPYLKMLQGLANGPGCAHYCFSLL
819 KL-AFSVTNNVIRLKPPSNVVSPLEQALSQHGAHGNNLIAVLAKYIYHKHDPALPRL 874	963 LHAVLEIIDSQQQDRYWCPPLLHRAAIAFLHALWQDRRDSAMLVLRTKPKF 1013	1100 SLLEY	1374 CFTSPPPEENPLVGFASIGDSSLYIILKKLLDFILKTGGG-FGRVRTHLYGSLLYYLQIA  1222 EMKVSDIPQXSQLVLNVCETLQEEVIALFDQTRHSLALGSATEDKDSM  1433 QRPDEPDTLEAAKKTWWERLTAPEDVFSKLQRENIALIESYGAALMEVVCRDAC  1270 ETDDCSRSRHRDQRGVCVLGLHLAKELCEVDEDGDSWLQVTRRLPILFTLLFTLEVSLR  1487 DGHEIGRMLALALDRIVSVDKQ-QQWLLYLSNSGYLKVLVDSLVEDDR	1330 MKQN	1653 SDŤÍQAILRCQDV-ŚAGSÍQĖLALITĠIİSKAA
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OKORMKOELSSELSTLLSSLSRYFRRGAPSSPATG 1717
                                                                            ---GLSTQAE-----GTRTLKSLLMFTM 1659
                           TDKISTAQKYVLARRRLVKVINNRAKLLSLCSFII 1897
                                                                                                                                                                                                                                                                                                                                                                                                                                                             292.5; DB 8; Length 2013;
No. 7.2e-13;
smatches 743; Indels 741; Gaps 104;
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|LLLAGEHQQPHFPGLTRGLVAVLL------- 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TWETHGNLMTERQVSRWFVQCLREQSMLLEIIFLY 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---LHQFAQDGLICQDMDCLMLTFGDIPH-HAPVL 327
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PTIMGSYLGVAHQRPPQRQVVLSKFVRQMGDLLPP 507
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YAYFEWAPSDLLVLTKMFKEQGFGSRQTNRHLVDETMDPFVDRIGYFSALILVEGMDI	236 ACQSPLGKEDTLLLIGHLEKVIVEANGSLDAVNLALLMALLNACFUI 281 284ESIHKCALDDRRELHOFAODGLICODMDCLMLTFGDIPH-HAPVL 327	SPIEQSTEERDDMIHQLPLLITERQYIATHSRLQDSQLWKLPGLQATUR	LAWALLRHTLNPEETSSVVRKIGGTAIQLNVFQYLFRLLQSLASGGNDCTTST	331 LAWALALKGISQLFDVIALAEFIEADEAWAELALADNVFLFLMESVVVSEIFIQEEF 38/ 381 ACMCVVGIISFVHTGREIHTGNOODTIDTACRVIADESID	YIRRVHNLITDFLALMPMKVKQLRNRADEDARMIHMSWQMGNEPPISLRRDLEHLMLLIG	422ELFWGTEPTSGLGILLDSVCGMFP 445	ELYKKNPFHLELALEYWCPTEPLQTPTIMGSYLGVAHQRPPQRQVVLSKFVRQMGDLLPP	446 HLLSPLLQLLRALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLMRRQTPKL 505     :   :   :   :     :	506 LYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSWTLFTCEIEMLLHVVSTADVIQH 565	535KVNGSSHVENIQGAGGSPVSWEHFFHSLMLYHEHLRKDLPSADSVQY 581	566 CORVKPIIDLVHKVISTDLSIADCLLPITSRIYMLLQRLTTVISPPVDVIASCVN 620	_	636 CSIPPVLKABLLKTLAAFGKSPBIAASLWQSLBYTQILQTVRIPSQRQAIGİBVB 690	666 GYGNLLMNSEQPQGEYGYTIAFLRITTLVKGQLGSTQSQGLVPCVMFVLKEMLP 720	721 SYHKWRYNSHGVREQIGCLILELIHAILNLCHETDLHSSHTPSLQFLCIGSL 772	746 RFRTRAYRRAABKWEVAEVVEVFYKLLRDYEPQLEDFVDQFVELQGEEII 796	773 AYTEAGQTVINIMGIGVDTIDMYMAAQPRSDGAEGQGQGLLIKTV 818	KI-AFSVTNNVIRLKPPSNVVSPLEQALSQHGAHGNNLIAVLAKXIYHKHDPALPRL		AIGLIKRLATVAPMSVYACLGNDAAA IRDAFLTRL		910 USAKEDWET-IKWAIDEFILVAN PALUKOLIELE TAMEN VAGASUGAKESDAMET SEL 92. 92. 1	LHAVLELIDSQQQDRYMCPPLLHRAAIAFLHALWQDRRDSAMLVLRTKPKF	1033 LHAILNILEKGTEGRTGPVAVRESPQLAELCYQVIYQLCACSDTSGPTWRYLRTSQDF 1090	1014 WENLTSPLEGILSPPSETS-EPSILETCALIMKIICLEIYYVVKGSLDQSLKDT 1066		GEGGIEDENRSVSGFLHEDTATKVRRKILNILDSIDFSQEIPEPLO
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1100 SLLEY-------QMLVSAWRML--LIIATTHADIMHLTD-SVVRRQLFLDV-- 1140
                                                                                                                                                                                                                                                                                                          1330 MKON------LHFTEATLHLLLTLARTQQGATAVAGAGITQSICLPLLSVYQLST 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1490 Q-----ACTSLLH----SRKMLQHYLQNKNGDGLPSAVAQRVQRPPSAASAAPSS 1535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1536 SKQPAADTEASEQQALHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLAEYNFLFA 1595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1596 LSFTTPTFDSEV------MLG 1626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : | | : : | | : : | | : : 1779 V.P.YNR.DGPRQDTQAPVVPYWRLPGLGIIIYLLKQSANDFFSYYDSHRQSVS 1838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1660 ENCFYLLISOAMRYLRDPAVH -- PRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATG 1717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1188 -----TIBILEGVLOADQQLMEKTKAKVFSAFITVLQMK 1221
                                                                                                                                                                                                                                                                                                                                                                       1222 E-----MKVSDIPQYSQLVL--NVCETLQEEVIALFDQTRHSLALGSATED---KDSM 1269
                                                                                                                                                                                                                                                                                                                                                                                                 1379 NGTAQTPSASR-KSLDAPSWPGVYRLSMSLMEQLLKTLRYNFLPEALDFVG-----VHQ 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1432 ERTLOCLNAVRIVOSLACLERADHIVGFILQLSNFMKEWHFHLPQLMR--DIOVNLGYLC 1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1627 EL------DXKKEPLTQAV-----GLSTQAE------GTRTLKSLIMFTM 1659
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                                           1201 LDFFDRAQIEQVIANCEHKNLRGQTVCNVKLLHRVLVAEVNALQGMAAIGQRPLLMEEIS 1260
                                                                                                                                                                                   1141 --LDGTKALLLVPASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGP------ 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1270 ETDDCSRSRHRDQRDGVCVLGLHLAKELCEVDEDGDSWLQVTRRLPILPTLLTTLEVSLR 1329
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Sequence 498, Application US/60717196
GENERAL INFORMATION:
APPLICANT: Mehdi MESRI et al.
TITLE OF INVENTION: STOWACH DISEASE TARGETS AND USES THEREOF FILE REFRENCE: CLOO1631
CURRENT APPLICATION NUMBER: US/60/717,196
CURRENT FILING DATE: 2005-09-16
NUMBER OF SEQ ID NOS: 2826
SOFTWARE: FESTEEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1718 VLPSPQGKSTSL---SKASPESQEPLIQL----VQAFVRHMQR 1753
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3.2%; Score 292.5; DB 8; Larity 18.9%; Pred. No. 7.2e-13; Conservative 303; Mismatches 743;
NKHWRRLLEGLSYYKPPSPSSAEKV-KANKDVASPLKELGLR               : : :           : : :       NALWRROPEAVHLLDKILKKHKPDFISLFKNPPKNVOHEKVOKASTEGVALGGOOGTR
ISKFLGLDEEQSVQLLQCYLQEDYRG-TRDSVKTVLQDERQSQALIL 
KIADYYYBERTCILRCVLHLL
**************************************
YAYFEMALEDILYLTKMFKEQGFGSROTINFHLVDETMDPFVDRIGYFSALILVEGNDI
ACQSPLGKEDTLLI
ESLHKCALDDRRELHQFAQDGLICQDMDCIMLTFGDIPH-HAPVL   :
LAWALLRHTLNPEETSSVVRKIGGTAIQLNVFQYLTRLLQSLASGGNDCTTST        ::  :
ACMCVYGLLSFVLTSLELHTLGNQQDIIDTACEVLADPSLP
BLFWGTEPTSGLGILDSVCGMFP ELYKKNPFHLELALEYWCPTEPLQTPTIMGSYLCVAHQRPPQRQVVLSKFVRQMGDLLPP
HILSPILQILRALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWRRQTPKL 
LYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSWTLFTCEIEMLLHVVSTADVIQH
CQRVKPIIDLVHKVISTDLSIADCLLPITSRIYMLLQRLTTVISPPVDVIASCVN
CLIVLAARNPAKVWIDLRHIGFLPFVAHPVSSLSQMISAEGMNAG
GYGNLIANSEQPQGEYGVTIAFIRLITTIVKGQLGSTQSQGLVPCVMFVLKEMLP 
SYHKWRYNSHGVREQIGCLILELIHAILNLCHETDLHSSHTPSLQFLCICSL:
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~ .	σ .	KL-AFSUTNNVIRLKPPSNVVSPLEQALSQHGAHGNNLJAVLAKYIYHKHDPALPRL 874   :: ::      :
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	875	
•	913	,
<b>~</b> 0	910	QSKIEDMRIKVMILEFLTVAVETOPGLIELF-LNLEVKDGSDGSKEFSLGMWSC 962 
	963	101
0	1033	YQLCAC
_	1014	WENLTSPLEGTLSPPSETS-EPSILETCALIMXIICLEIYYVVKGSLDGSLKDT 1066
•	1001	LFSQLQYLPFSNXEYEISMLNQMSWLMKTASIELRVTSLNRQRSHTQRLL 1140
_	1067	IKKRSIEKRFAYWSGY1082
•	1141	HILLDDMPVKPYSDGEGGIEDENRSVSGFLHFDTATKVRRKILNILDSIDFSQEIPEPLQ 1200
_	1083	SSCT 1099
0	1201	LDFFDRAQIEQVIANCEHKNLRGQTVCNVKLLHRVLVAŠVNALQGMAAIGQRPLLMEEIS 1260
_	1100	SLLEY
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_	1141	LDGTKALLLVPASVNCLRLGSMKCTLLLILRQWKRELGSVDEILGP 1187
•	1321	KILDDEAAQELMPVVAGAVFTLTAHLSQAVLTEQKQTSVLGPAEAHYAFMLDS 1373
_	1188	
•	1374	CFTSPPPEBNPLVGFASIGDSSLYIILKKLLDFILKTGGG-FQRVRTHLYGSLLYYLQIA 1432
	1222	EMKVSDIPQYSQLVLNVCETLQEEVIALFDQTRHSLALGSATEDKDSM 1269
	1433	QRPDEPDTLEAAKKTWWERLTAPEDVFSKLQRENIAIIESYGAALMEVVCRDAC 1486
_	1270	HRDQRDGV
	1487	DGHEIGRMLALALLDRIVSVDKQ-QQWLLYLSNSGYLKVLVDSLVEDDR 1534
	1330	IMFTEATLHLLITARTQQGATAVAGAGITQSICLPLLSVYQLST 137
0	1535	TLÓSILIPQPPILKALYTYÉSKWAFÜTRVÁKIÓGĞALBILKSGVIVRÍAQCQVYDMRP 1592
	1379	NGTAQTPSASR-KSLDAPSWPGVYRLSMSLMBOLLKTLRVNFLPEALDFVGVHQ 1431
•	1593	ETDPQSMFGMRDPPMFIPTPVDRYRQILLPALQLCQVILTSSMAQHLQAAGQVLQFLISH 1652
<b>5.</b>	1432	FMKEWHF
٥	1653	SDTIQAILRCODV-SAGSLOELALLTGIISKAALPGILSELDVVNEGSLM 1702
>-	1490	QACTSLIHSRKWLQHYLQNKNGDGLPSAVAQRVQRPPSAASAAPSS 1535 :
٥	1703	ELQGHIGRRQRQCLGLLSRFGGSDRLRQFKFQDDNVEGDKV 1743
>-	1536	SKQPAADTEASEQQALHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLAEYNFLFA 1595   : :   :
0	1744	177
_	1596	LSFITPTPDSEVMLG 1626
	1779	VCLFTPSLSETVNRDGPRQDTQAPVVPYWRLPGLGIIIYLLKQSANDFFSYYDSHRQSVS 1838
<u>~</u>	1627	ELDKKKEPLTQAVGLSTQAEGTRTLKSLLMFTM 1659

506 LYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSWTLFTCEIEMLLHVVSTADVIQH 565  537KVNGSSHVENIQGAGGSPVSWEHFPHSLALYHEHLRKDLPSADSVQY 583  566 CQRVKPIIDLVHKVISTDLSIADCLLPITSRIYMLLQRLTTVISPPVDVIASCVN 620  621 CLTVLAARVPAKVWTDLRHTGFLPFVAHPVSSLSQMISAEGANAG 665  638 CSIPPVLKABLLKTLAAFGKSFBIAASLWGSLGSTQGICPVPVVILGLLQ 637  639 CSIPPVLKABLLKTLAAFGKSFBIAASLWGSLGSTQGICPVPVWFVLKEMLP 720  640 GYGNLLMNSEQPQGEYQTIAFLRITTLVKGQLGSTQSQGLPVPVWFVLKEMLP 720  651 GYGNLLMNSEQPQGEYQTIAFLRITTLVKGQLGSTQSQGLPVPVWFVLKEMLP 720  652 GYGNLLMNSEQPQGEYGTIAFLELITALLNCHETDLHSSHPGFDPYLQFLRBSVFL 747  721 SYHKWRYNSHGVREQIGCLILELIHAILNLCHETDLHSSHPSGLDFVDQFVELQGEBII 798  773 AYTEAG		1188
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	8 6 8 6 8 6 8 6 8 8 8 8 8 8 8 8 8 8 8 8	6 B 6 B 6 B 6
DD 1839 KLONVEQLPPDEIKE-LCGSVWPAGVDKISTAQKYVLARRRLVKVINNRAKLISLGSFII 1897  OY 1660 ENCFYLLISQAMRYLRDPAVHPRDKQRKQELSSELSTLLSSLSRYFRRGAPSSPATG 1717  DD 1898 ETCLFILWHILEYYLHCMPTDSQDSLFPASRTLGDSFAS- 1942  OY 1718 VLPSPQGKSTSLSKASPESQEPLIQLVQAFVRHWQR 1753  1718 VLPSPQGKSTSLSKASPESQEPLIQLVQAFVRHWQR 1753  DD 1943ETNLDFRSGLAIVSQHDLDQLQADAINAFGESLQK 1977  RESULT 10  NS-60-64-936-323  GENERAL INFORMATION: APPLICATION: APPLICATION: APPLICATION WUMBER: US/60/664,936  CURRENT APPLICATION NUMBER: US/60/664,936  CURRENT PILLING DATE: 2005-03-25  NUMBER OF SEQ ID NOS: 2456  SOFTWARE: FABLESQE FOR Windows Version 4.0  SEG ID NO 323  LENGTH: 2014  TYPE: PRT  T	Query Match   3.2%;   Score 292.5;   DB 8;   Length 2014;     Best Local Similarity   18.3%;   Pred. No. 7.2e-13;     Matches   417;   Conservative   302;   Mismatches   745;   Indels   739;   Gaps   104;     Al NKHWRRLEGG	381 ACMCVYGLLSFVLTSLELHTLGNQODIIDTACEVLADPSLP

YAYFEMAPSDLLVLTKMFKEQGFGSRQTNRHLVDETMDPFVDRIGYFSALILVEGMDI  ACOSPLGKEDTLLLIGHLERVTVEANGSLDAVNLALLMALLYCFDI	390 YIRRVHNLITDFLALMPMKVKOLKNRADEDARMIHMSMQMGNEFFISLKKULLEHLALLIG 449 422		SYHKWYNSHOWEGICCLIEELHAALINLCHEIDLHSSHIED	875 AIQLIKRLATVAPMS	963 LHAVLELIDSQQQDRYWCPPLLHRAAIAFLHALWQDRRDSAMLVLRTKPKF 1013
8 8 8 8 8 8 8	8 8 8 8 8 8 8	8 6 8 6 8	868686	8 8 8	6 8 6 8 6 6
	Qy         1536 SKQPAADTEASEQQALHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSLDLAEYNFLFA 1595           Db         1746 SKKDEIEL-AMQQICANVMEYCQSLMLQSSPTFQHA 1780           Qy         1596 LSFTTPTFDSEV	Db 1900 ETCLFILWRHLEYYLLHCMPTDSQDSLFASRTLFKSRRLQDSFAS- 1944  Qy 1718 VLPSPQGKSTSLSKASPESQBPLIQLVQAFVRHWQR 1753	# APPLICANT: JOSELOFF, Elizabeth et al. TITLE OF INVENTION: KIDNEY DISEASE TARGETS AND USES THEREOF FILE REFERENCE: CL001616 GURRENT APPLICATION WUNBER: US/60/701,038 CURRENT FILING DATE: 2005-07-21 NUMBER OF SEQ ID NOS: 1828 SOFTWARE: FastSEQ for Windows Version 4.0 LENGTH: 2015 TYPE: PRT GRANISM: Homo sapiens US-60-701-038-308	Query Match 3.2%; Score 292.5; DB 8; Length 2015; Best Local Similarity 18.9%; Pred. No. 7.2e-13; Matches 417; Conservative 302; Mismatches 745; Indels 739; Gaps 41 NKHWRRLLEGLSYYKPPSPSSAEKV-KANKDVASPLKELGLR	DD 26 NALWERQPEAVHILDKILKKHRPDFISLEKNPPRNVQQHEKVQKASTEGVAIQGQGGTRL 85  QY 82ISKFLGLDEEQSVQLLQCYLQEDYRG-TRDSVKTVLQDERQSQALIL 127  B6 LPEQLIKEAFILSDLFDIGELAAVELLLAGEHQPHFPGLTRGLVAVLL 134  QY 128 KIADYYEERTCILRCVLHLLTYFQDERHPYRVEYADCVD 167

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                                                                                                                                                                    ORPDEPDTLEAAKKTMWERLTAPEDVFSKLORENIAIIE-----SYGAALMEVVCRDAC 1488
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ELQCHIGRFQRQCLGLLSRFGGSDRLRQFKFQDDNVEG-------DKV
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                      -OMLVSAWRML--LIIATTHADIMHLTD-SVVRRQLFLDV--
                                                                            -------TEILEGVLQADQQLMEKTKAKVFSAFITVLQMK
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                                                                                                                                                                                                            DGHEIGR-------MLALALLDRIVSVDKQ-QQWLLYLSNSGYLKVLVDSLVEDDR
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                                                              --LDGTKALLLVPASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGP-
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                                                                                                                                                                                                                                                                                                      226 YAYFEMAPSDLLVLTKMFKEQGFGSRQTNRHLVDETMDP--FVDRIGYFSALILVEGMDI
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                                                                        Indels 739;
                                                Length 2015;
                                                Query Match
3.2%; Score 292.5; DB 8;
Best Local Similarity 18.9%; Pred. No. 7.2e-13;
Matches 417; Conservative 302; Mismatches 745;
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-717-251-663
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DD 1537 TLQSLLTPQPPLLKALYTYESKMAPLTRVAKIQOGAN  Qy 1379 NGTAQTPSASR-KSLDAPSWPGVYRLSMSLMEQLLKT  DD 1595 ETDPG/SMFGMRDPPMFIPVDRYRQILLPAL/LC/LOLANTWRQULPPUDRYRQILLPAL/LC/LOLANTWRQULPPUDRYRQILLPAL/LC/LOLANTWRQULPPUDRYRQILLPAL/LC/LSNFWW  QY 1430 QACTSLLHSRKMLQHYLQNKNGE  DD 1705 ELQCHIGRPGRQCLGLLSRPGGSDBLRGPKPGDDDNVP  DD 1736 SKQPAADTEASEQALHTVQYGLKILSKTLAALRHP  QY 1536 SKQPAADTEASEQALHTVQYGLKILSKTLAALRHP  DD 1746 SKKDEIEL-AMQQICANVMEY	RESULT 14 US-60-664-936-324  Sequence 324, Application US/60664936 GENERAL INFORMATION: TITLE OF INVENTION: KIDNEY DISEASE TARGETS AND UPTER PILE REFERENCE: CLO01591 CURRENT PILING DATE: 2005-03-25 WUMBER OF SEQ ID NOS: 2456 SOFTWARE: FASTSEQ for Windows Version 4.0 SOFTWARE: FASTSEQ for Windows Version 4.0 SOFTWARE: FASTSEQ for Windows Version 4.0 SOFTWARE: PAST CURRENT FILING SOFTWARE: PAST CURRENT FILING SOFTWARE: PAST CONGRANISM: Homo sapiens US-60-664-936-324 MATCH 2012  MATCH 2012  MATCH 2012  A NEWRITH 18.94; Pred. NO. 8.6e-15 Best Local Similarity 18.94; Pred. NO. 8.6e-15 MATCH 416; Conservative 302; Mismatches 7.7  DD 26 NALWERQPEAVHLLDKILKKHKPPFISLFKNPPRNVV OY 82ISKFLGLDEGCSVQLLCCYLQED) OY 128 KIADYYVEBETCILRCVHLL
	963 LHAVLELIDSQQORYWCPPLHRAAIAFLHALMQDRRDSAMLVLRTKFKF 1013 1035 LHANIALEKGTEGRTGVYAVREABOALGECCSDTSGPTMYLKTSQDF 1092 1014 WENLTSPECTISPPSETS-EPSILETCALIMKIICLEITYVVKGSLDGSLKOT 1066 1093LESQLQYLPPSNKEYEISMLNQMSWLMKTASIELRYTSIARQRSHTQRLL 1142 1067LEKKFSIEKREAYWGGY
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qq	1537	TLQSLLTPQPPLLKALYTYESKMAFLTRVAKIQQGALELLRSGVIVRLAQCQVYDMRP 1594
ò	1379	NGTAQTPSASR-KSLDAPSWPGVYRLSMSLMEQLLKTLRYNFLPBALDFVGVHQ 1431
	1595	:   :   :   :   : ETDPQSMFGMRDPPMFIPTPVDRYRQILLDPALQLCQVILTSSMAQHLQAAGQVLQFLISH 1654
ò	1432	ERTLOCLNAVRTVQSLACLEBADHTVGFILQLSNFMKEWHPHLPQLMRDIQVNLGYLC 1489
qq	1655	ELALLTGIISKAALPG
	0 1	QACTSLIHSRKMLQHYLQNKNGDGLPSAVAQRVQRPSAASAAPSS 1535
		PDVCOTTI-DOST-DLAEYNFLFA 159
; A	746	178
	1596	LSPTTPTFDSEVMLG 1626
	1781	:   : :   : :   : : : : : : : : : : : :
ò	1627	ELDKKKEPLTQAVGLSTQAEGTRTLKSLLMFTM 1659
qa	1841	:  KLQNVEQLPPDEIKE-LCQSVMPAGVDKISTAQKYVLARRRLVKVINNRAKLLSLCSFII 1899
ò	1660	ENCFYLLISQAMRYLRDPAVHPRDKQRWKQELSSELSTLLSSLSRYFRRGAPSSPATG 1717
Ωp	1900	ETCLFILWRHLEYYLLHCMPTDSQDSLFASRTLFKSRRLQDSFAS- 1944
ò	1718	VLPSPQGKSTSLSKASPESQEPLIQLVQAFVRHMQR 1753
qq	1945	ETNLDFRSGLAIVSQHDLDQLQADAINAFGESLQK 1979
ESULT 14 S-60-664 Sequence GENERALIC APPLIC TITLE FILE F CURREN CURREN NUMBER SOFTWA SEQ ID LENGT TENGT	1-36-324, A INFORMATIONAL INFORMATIONAL INFO	TERRICE S
US-60-664	-936-	324
Query Match Best Local S Matches 416	atch cal S	3.2%; Score 291.5; DB 8; Length 2012; Similarity 18.9%; Pred. No. 8.6e-13; .6; Conservative 302; Mismatches 744; Indels 741; Gaps 104;
Š	41	NKHWRRLLEGLSYYKPPSPSSAEKV-KANKDVASPLKELGLR- 81
qq	26	NALWRRQPEAVHLLDKILKKGHKPDFISLFKNPPKNVQQHEKVQKASTEGVAIQGQGTRL 85
È	83	QDERQSQALIL 12
QQ Q	98	LPEQLIKEAFILSDLFDIGELAAVELLLAGEHQQPHFPGLTRGLVAVLL 134
à à	128	TAD
g	CFT	
È	168	GNLMTERQVSRWFVQCLREQSMLLEIIFLY 22
d d	189	23
δ	226	YAYFEMAPSDLLVLTKMFKEQGFGSRQTNRHLVDETMDPFVDRIGYFSALILVEGMDI 283

Db 856 Qy 875 104;	81 Qy 910 85 Db 973 127 Qy 963	Db 1033 LF Cy 1014 WE Db 1093 LF Cy 1014 WE Db 1091 188		71 281 Qy 1100 SI 72 327 Db 1261 Ti 73 330 Qy 1141	380	421 Db 1374	445	505 CY 1270 534 Db 1487	H 565 L30 M : Db 1535 M 27 581 CV 1379 M	620 CJ 635 Db	NG 665 Db 1653 SI 690 Cv 1490 D	720 Db 1703 745	772 OY 1536 796 Db 1744	TV 818 CY 1259 CY 1596 C C C C C C C C C C C C C C C C C C C
.2%; Score 291.5; DB 8; Length 2012; .9%; Pred. No. 8.6e-13; Pred. No. 9.6e-13; Gaps	LSYXKPPSPSSAEKV-KANKDVASPLKE	LPEQLIKEAFILSDLFDIGELAAVELLIAGEHQQPHFPGLTRGLVAVLL	KLEKELVSKYRQQFEELYKTEAPTWETHGNLMTERQVSRWFVQCLREQSMLLEIIFLY          :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :   :     :   :     :   :     :     :            YAYFEMAPSDLLVLTKMFKEQGFGSRQTNRHLVDETMDPFVDRIGYFSALILVEGMDI	ACQSPLGKEDTLLLIGHLERVIVEANGSLDAVNLALLMALLICFULESLHKCALDDRRELHQFAQDGLICQDMDCLMLTFGDIPH-HAPVL	328 LAWALLRHTLMPEETSSVVRKIGGTAIQLMVFQYLTRLLQSLASGGNDCTTST	381 ACMCVYGLLS-FVLTSLELHTLGNQODIIDTACEVLADPSLP381	422ILIDSVCGMFPGLGILIDSVCGMFP 	HILSPLLQLIRALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWRRQTPKL 	LYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSWTLFTCEIEMLHVVSTADVIQH :	CQRVKPIIDLVHKVISTDLSIADCLLPITSRIYMLLQRLTTVISPPVDVIASCVN	CLIVLAARNPAKVWIDLRHIGFLPFVAHPVSSLSOMISAEGMNAG	GYGNLLMNSEQPQGEYGYTIAFLRITTLVKGQLGSTQSQGLVPCVMFVLKEMLP	721 SYHKWRYNSHGVREQIGCLILELIHAILNLCHETDLHSSHTPSLQFLCICSL :	773 AYTEAGQUINIMGIGYDTIDWVMAAQPRSDGAEGGGGGLIKTV
; ORGANISM: Homo sapiens US-60-701-038-307 Query Match Best Local Similarity 18.9%; Matches 416; Conservative 3	(5) 45 1	LPEQLIKEAF KIADYYYEER  ::::		236 ACGSPLGKEDTLLLI 284ESLHKC : : : 282 SFIEQSTEERDDMIHQL	328 LAWALLRHTLNPE	381 ACMCVYGLLSFVI  :  :: 388 YIRRVHNLITDFLAI	422	446 HLLSPLLQLLRALVSGKSTAKKVYSFL :    :	506 LYPLGGQTNLRIPQ :   ::   535KVNGSSHVENIQ	566 CQRVKPIIDLVHKV.   :   582RHLPSRGIIQK-	621 CLTW       636 CSIPPVLKAELLKTI	666 GYGNLLMNSEQPQGI       1   691LNEIESRCEI	721 SYHKWRYNSHGVRE : 746 RFRTRAYRRAEKW	773 AYTEAG 
CRGAN US-60-701 Query M Best Lo Matches	දු පු ද	4 & B	8 & B & S	2	<i>&amp;</i> 8	රු සි	රු දු	ço da	oy oy	රු අ	දු දු	<u>ک</u> و	. & A	oy Gb

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>-	875	AIOLLKRLATVAPMS
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>	910	OSKIEDMRIKVWILEFLTVAVETOPGLIELF-LNLEVKDGSDGSKEFSLGMWSC 962
۵	973	EKKLVAIÄHETRIHİLNLLITSLECNPPNLALYLLGFELKKPVSTTNLQDPGVLGCPRTC 1032
د ح	963	LHAVLELIDSQQQDRYWCPPLLHRAAIAFLHALWQDRRDSAMLVLRTKPKF 1013
a :	1013	
× .a	1001	
· >-	1067	LKKKSIEKRFAYWSGY1082
Ω	1141	:   :   H         H   HLLLDDMPVKPYSDGEGGIEDENRSVSGFLHFDTATKVRRKILNILDSIDFSQEIPEPLQ 1200
>-	1083	SSCT 1099
Д	1201	LDFFDRAQIEQVIANCEHKNLRGQTVCNVKLLHRVLVAEVNALQGMAAIGQRPLLMEEIS 1260
>-	1100	SLLEYQMLVSAWRMLLIATTHADIMHLTD-SVVRRQLFLDV 1140
Д	1261	TVLQYVVGRNKLLQCLHAKRHALESWRQLVBILLTACPQDLIQAEDRQLIIRDILQDVHD 1320
>-	1141	TGSADEITGB
д	1321	
۸	1188	
д	1374	CFTSPPPEENPLVGFASIGDSSLYIILKKLLDFILKTGGG-FQRVRTHLYGSLLYYLQIA 1432
<b>&gt;</b>	1222	
Q	1433	QRPDEPDTLEAAKKTMWERLTAPEDVFSKLQRENIAIIESYGAALMEVVCRDAC 1486
2 ح	1270	ETDDCSRSRHRDQRDGVCVLGLHLAXELCEVDEDGDSWLQVTRRLPILPTLLTTLEVSLR 1329  1
a >	1330	137
<u>م</u> ج	1535	TLOSILITPOPPLIKALYTYESKARFLIRVAKIQOGALELIRSGVI VRLAQCOVYDWRP 1592
<u>~</u>	1379	NGTAQTPSASR-KSLDAPSWPGVYRLSMSLMBQLLKTLRYNFLPBALDFVGVHQ 1431
ą	1593	ETDPQSMFGMRDPPMFIPTPVDRYRQILLPALQLCQVILTSSMAQHLQAAGQVLQFLISH 1652
<b></b>	1432	FHLPQLMRDIQVNLGYLC
q	1653	SDÍIGAILRCQDV-SAGSÍQELALLTGIISKAALPGILSELDVDVNEGSLM 1702
Ā	1490	SAVAQRVQRPPSAASAAPSS 153
ភ្	1703	
Ş.	1536	
ą	1744	SKKDEIEL-AMQQICANVWEYCOSLMLQSSPTFQHA 1778
≱.	1596	LSFTTPTFDSEVMLG 1626
ą	1779	VCLFTPSLSETVNRDGPRQDTQAPVVPYWRLPGLGIIIYLLKQSANDFFSYYDSHRQSVS 1838
<u>≽</u> .	1627	BLGISTOAV
ð	1839	1839 KLONVEQLPPDEIKE-LCQSVMPAGVDKISTAQKYVLARRRLVKVINNRAKLLSLCSFII 1897

1660 ENCEYLLISQAMRYLRDPAVHPRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATG 1717	1898 ETCLFILWRHLEYYLLHCMPTDSQDSLFASRTLFKSRLQDSFAS- 1942	1718 VLPSPQGKSTSLSKASPESQEPLIQLVQAFVRHMOR 1753	1943ETNLDFRSGLAIVSQHDLDQLQADAINAFGESLQK 1977
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